



IL-1 $\alpha$

SNP #	GTC Location	Base # in IL-1 $\alpha$ gene	Relative to +1	Region	cDNA	Location	AA#	Mutation	Type	%	SNP Sequence	SNP ID
1	2346	1553	-3885	343903		Promoter			C/T	C=98% T=2%	GCAATGAGCCACGGCACCAGCCACT	1
2	2467	1674	-3764	343782		Promoter			C/T	C=62 T=38	TGAACATAGAACTCAAGAAATTTGA	2
3	2505	1712	-3726	343744		Promoter			T/C	T=98 T=2	CACACTCTCAITATGAAATCTCCAT	3
4	2623	1830	-3608	343626		Promoter			G/A	G=62 A=38	CATATCTGGGAGACCTTCAATAAA	4
5	3116	2323	-3115	343133		Promoter			C/T	T=74 C=26	AAAAATTATGTTTTTCTCTTCATTCA	5
6	3475	2682	-2756	342774		Promoter			C/T	C=66 T=34	TCTTTATAAGCCATCACTTGGTG	6
9	3962	3169	-2269	342287		Promoter			G/A	G=70 A=30	CGAGAGGTGGGTGCCTGAAGCCACC	7
10	4113	3320	-2118	342136		Promoter			C/T	C=98 T=2	TGTTACACAGTCCCAGAAAGCGGGC	8
11	4725	3932	-1506	341504		Promoter			C/T	C=68 T=32	TAAAGAGGAAACCAAGGTAAGCAGA	9
12	5029	4236	-1202	341220		Promoter			C/T	C=78 T=22	ACACAAAGCTGCTTTCTCCAGATC	10
13	5342	4549	-889	340907		Promoter			C/T	C=72 T=28	CCAGGCAACAACCATTTGAAGGCTC	11
14	6377	5583	+145	340907		Intron 1			C/T	C=78 T=22	AAAGCTACAGCCTCTCCTTCTTT	12
15	6483	5689	+251	339766		Intron 1			T/A	T=66 A=34	CTGATTCGTTTACTGAGGGACG	13
16	6495	5701	+263	339754		Intron 1			G/A	G=70 A=30	ACTGAGGACGGCAGAACTAGTTTC	14
17	8099	7302	+1864	338150		Intron 3			A/C	A=66 C=34	CTTGAATCTTAAATACTTTTGT	15
18	8127	7330	+1892	338122		Intron 3			G/A	G=72 A=28	CTCAGTAGAGGTCCAGAGACCT	16
19	9058	8260	+2822	337191	290	Exon 4	85	R to Q	G/A	G=98 A=2	AAGAAGAGACGGTTGAGTTT	17
24	10950	10153	+4718	335286		Intron 4			A/C	A=78 C=22	TCTGGATTGGVAATAATTCCTA	18
25	10963	10166	+4728	335286		Intron 4			T/C	T=72 C=28	ATTCTAATAATCCCTCCAG	19
26	11079	10282	+4845	335170	376	Exon 5	114	A to S	G/T	G=72 T=28	GCCTAGGTCA/GCACCTTTTAG	20
30	12864	12065	+6627	333385		Intron 6			G/C/A	G=38 C=36 A=26	GCCCCACCTGCCCCACCCCA	21
31	15191	14249	+8811	331038		Intron 6			A/C	A=68 T=32	CCTTTTCTAAGATCTTGTTCTCTA	22
32	15840	14898	+9460	330409	1260	Exon 7 3' UTR			G/A	A=74 G=26	TTTGCCCTTCTACTTTTAAAGTT	23
33	15993	15051	+9613	330256	1440	Exon 7 3' UTR			C/T	T=72 C=28	AAATACTTCTTTGAAGCCGAGC	24
34	16129	15187	+9749	330120	1549	Exon 7 3' UTR			C/G	C=96 G=4	CTGAGTGTGAACGAGGCATCCTC	25

FIGURE 8

# IL-1β

SNP #	GTC Location	Base # in IL-1β gene	Relative to +1	Region	cDNA	Location	AA#	Mutation	Type	%	SNP Sequence	SEQ ID NO
1	1824	770	-5164	397483		Promoter			C/T	C=84 T=16	GCCTGGGTCC/CAGACTTGACAAA	26
2	3029	1975	-3959	396278		Promoter			T/C	T=96 C=4	AGAAAAGACATAGAGTAGGA	27
3	3095	2041	-3893	396212		Promoter			G/A	G=70 A=30	TCCAAAGGAA/IGGACAAAGGTC	28
4	3243	2189	-3745 (-3737)	396063		Promoter			C/T	C=62 T=38	GGGAGGAGAA/TGGAA/TGTGCCCTTGGACTCT	29
5	3302	2248	-3686	396005		Promoter			A/G	A=98 G=2	GAAGAAAGCCCA/TTGAGATGATG	30
6	3734	2680	-3254	395573		Promoter			T/C	T=96 C=4	GATAACTGGCTGCGAAAGCCCATGAT	31
7	4083	3029	-2905	395224		Promoter			A/G	A=98 G=2	GGAAAGACAGGATCTGATACATAC	32
8	4594	3540	-2394	394713		Promoter			G/A	G=98 A=2	CCTGTCACTGCGCTTGTGATCCTCCTT	33
9	4610	3556	-2378	394697		Promoter			G/A	G=96 A=4	ATCCTCCTTCGTTTCAGCTTGTAAATC	34
10	5521	4464	-1470 (-1464)	393786		Promoter			G/C	G=70 C=30	CACTCCCTTGIGATAAATGCAGAGCGAG	35
14	6490	5423	-511	392837		Promoter			T/C	T=54 C=46	AGAGAGCTCCTTGAGGCGAGAGAAC	36
15	6970	5903	-31	392337		Promoter			C/T	C=54 T=46	TTTTGAAAAGC/CATAAAAACAGCGAGGGAG	37
17	7046	5979	+45	392261	45	Exon 1 5' UTR			T/C	T=54 C=46	GCTCTGGGAT/TCTCTTTCAGCCCAATCTTCAT	38
19	7750	6680	+746	391557		Intron 2			C/T	none	ACTACTTTC/CATTACAAGTCCCTCCAG	39
24	10888	9810	+3876	388419		Intron 4			G/A	G=64 A=36	AAATTTTGGC/CAGCTCGCCTCACGAG	40
25	10965	9887	3953	388342	401	Exon 5	105	F to F	T/C	C=78 T=22	CTATCTTCTTCGACACACATGGGATAACG	41
30	12561	11482	+5548	386746		Intron 6			G/A	G=78 A=22	CCCTCTCCCG/GCCCCCATCCCTAGG	42
35	13517	12440	+6506	385790	997	Exon 7 3' UTR			C/A	C=98 A=2	ATAGCCTGGA/CITTCCTGTGTCT	43
37	13921	12845	+6911	385386	1401	Exon 7 3' UTR			G/C	G=78 A=22	CTTTAATTAA/GACTGAAAATATATAAGC	44
38	14233	13148	+7214	385074					C/T	C=84 T=16	CAGTGCACATCTCGAACAGGATC	45

FIGURE 9

# IL-1 RNic

SNP #	GTC Location	Base # in IL-1 RN Gene	Relative to +1	Region	cDNA	Location	AA#	Mutation	Type	%	SNP Sequence	SEQ ID NO
14	2189	11268	-4864	669240					G/A	G=86 A=14	GTTGGGTCAC\GTACCCGACGTGCTA	46
15	2251	11330	-4744	669277					T/G	T=76 G=24	ACTGTTACACATAGCCCAAGATATGGA	47
18	3332	12412	-3662	670358					T/G	T=56 G=4	TGTTTGCTTGTCTCTCTCTCTCAGC	48
19	3576	12657	-3417	670602					A/G	G=80 A=20	AGCTGGGCTCTGTGAGTTGTGGTGGC	49
21	3763	12844	-3230	670789					C/T	C=82 T=18	GTGTGTGTCTGTGTGTGTGTGTGTG	50
22	3803	12886	-3188	670829					G/A	G=98 A=2	GAGAGAAATGA\GAAATATATGAGTGGTGG	51
25	4543	13626	-2448	671580					T/C	C=78 T=22	TATCTTGCTCTCCCATTCCTGATGC	52
26	4648	13731	-2343	671674					T/C	T=98 C=2	GTCAACCATCA\TTGGGGTTGTGGATC	53
29	5534	14616		672560		Promoter			C/T	C=98 T=2	TGAGCCAAGG\CGGAAGAGAACAGGA	54
30	5992	15073	-1002	673020		Promoter			T/C	T=74 C=26	GCAGATAGCA\TCAGGTCCATTTTTC	55
31	6493	15573	-501	673519		Promoter			G/C	G=70 C=30	CTCTCAGAGA\GGGCTTCCCTGGCCA	56
32	6494	15574	-500	673520		Promoter			G/A	G=98 A=2	TCTCAGAGAG\GGCTTCCCTGGCCAC	57
33	6606	15686	-388	673632		Promoter			C/T	C=70 T=30	TATTTTATTTG\CTAACTTGTTCCTTG	58
34	6742	15822	-252	673768		Promoter			A/C	A=70 C=30	GCACACATGC\ATGAGCTGGCGGCAG	59
35	6953	16033	-41	673979		Promoter			G/A	G=70 A=30	GGGAGGGGAG\GCTGGGCTCCTCCTT	60
36	7034	16114	+40	674060	36	Exon 1 5' UTR			G/A	G=70 A=30	CCCAGGTACT\GCCCGGGTGCTACTT	61
37	7090	16170	+96	674116	92	Exon 1 5' UTR			G/A	G=74 A=26	GGAAGACCTC\GGGAAGACCTCCTGTC	62
38	7109	16189	+115	674135	111	Exon 1 5' UTR			G/C	G=70 C=30	CCTGTCCTAT\GAGGGCCCTCCCCATG	63
39	7156	16235	+162	674182		Intron 1			T/C	T=70 C=30	TCATATTTT\TCACCTGAGAAATGA	64
40	7298	16378	+304	674324		Intron 1			A/G	A=70 G=30	GGAGGCATCC\ATGGGAGACCATGCA	65
42	9021	18100	+2027	676047		Intron 1			G/T	G=80 T=20	GTGCATACTC\GGACTGGAAACTGGA	66
43	9064	18143	+2060	676090		Intron 1			G/C	G=70 C=30	AAAGGATAGA\GATGGAACCATGTGC	67
44	9239	18316	+2245	676265		Intron 1			A/C	A=70 C=30	AGGGTAAAT\TATTTTATGGATCCAA	68

FIGURE 10A

# IL-1 RNic (Continued)

SNP #	GTC Location	Base # in IL-1 RN Gene	Relative to +1	Region	cDNA	Location	AA#	Mutation	Type	%	SNP Sequence	SEQ ID NO
61	18726	27810	+11732	685752	239	Exon 3	39	A to A	T/C	T=72 C=28	AACTAGTTGC/TGGATACTTGCAAGG	69
62	18781	27865	+11787	685807		Intron 3			T/C	T=74 C=26	GCCAGGAAAGTCAATGTATGTGGGC	70
63	18792	27876	+11797	685818		Intron 3			G/A	G=72 A=28	CAATGTATGTGGGCATCAGTCACT	71
64	18813	27897	+11819	685839		Intron 3			G/C	G=72 C=28	CACTTTGGCCG/TCTGTCTGCAGCAG	72
65	18841	27938	+11860	685880		Intron 3			T/G	T=88 G=12	TGCACAAACCC/TAGGTCATGTCTTAATC	73
66	18857	27941	+11855	685903		Intron 3			A/C	A=72 C=28	AAACCCTAGGTGCAATGTCTTAATC	74
67	18892	27975	+11890	685918		Intron 3			T/C	T=96 C=4	TGTATTCAAGTTTGAAAGCTGGGAGG	75
68	18895	27979	+11892	685921		Intron 3			G/A	G=98 C=2	ATTCAGTTTGAAAGCTGGGAGGGCC	76
76	20075	28987	+13070	687101		Intron 3			G/A	G=74 A=26	AAAAATACCC/GGGGTCTCTTCATTTA	77
77	20097	29010	+13092	687123		Intron 3			T/C	T=70 C=30	TTATTGCTGC/TTCTCTTCTATTAA	78
78	20311	29224	+13307	687337		Intron 3			A/T	A=78 T=22	AAACAACCA/AAATTTTCTTATGA	79
79	20418	29331	+13414	687444		Intron 4			T/A	T=58 A=42	GCAGAGTGC/TTGGCTTGCCTGGGC	80
80	20524	29436	+13520	687550		Intron 4			T/G	T=76 G=24	GCATGGCGGCTGACTTCCAAAAGGG	81
81	20579	29491	+13575	687605		Intron 4			G/A	G=50 A=50	CGCTTATTATGACTTCTGCTTGCA	82
82	20618	29531	+13614	687644		Intron 4			C/T	C=70 T=30	AAGCCAGTCA/CGTGGCTAAGTCTAG	83
89	21822	30735	+14818	688848	458	Exon 4	112	S to S	T/C	T=60 C=40	GCTCAGACAG/TGGCCCCACCACCAG	84

FIGURE 10B

# IL-1 RNsec

SNP #	GTC Location	Base # in IL-1 RN gene	Relative to +1	Region	cDNA	Location	AA#	Mutation	Type	%	SNP Sequence	SEQ ID NO
61	18726	27810	2014 (+2018)	685752	194	Exon 2	57	A to A	T/C	T=72 C=28	AACTAGTTGCTGGATACTTGCAAGG	85
62	18781	27865	2069	685807		Intron 2			T/C	T=74 C=26	GCCAGGAAAGTCAATGTATGTGGGC	86
63	18792	27876	2080	685818		Intron 2			G/A	G=72 A=28	CAATGTATGTGGGCATCAGTCACT	87
64	18813	27897	2101	685839		Intron 2			G/C	G=72 C=28	CACCTTGCCCGTCTGTCTGCAGCAG	88
66	18857	27938	2142	685903		Intron 2			A/C	A=72 C=28	AAACCCTAGGTGC\AAATGCTCTAATC	89
67	18892	27976	2180	685918		Intron 2			T/C	T=96 C=4	TGTATTCAAG\TTTGAAGCTGGGAGG	90
68	18895	27979	2183	685921		Intron 2			G/A	G=98 C=2	ATTCAAAGTTTGAAGCTGGGAGGGCC	91
76	20075	28988	3192	687101		Intron 2			G/A	G=74 A=26	AAAAATACCC\GGGGTCTCTTCATTA	92
77	20097	29010	3214	687123		Intron 2			T/C	T=70 C=30	TTATTGCTGC\TTCTCTTCTATTAA	93
78	20311	29224	3428	687337		Intron 2			A/T	A=78 T=22	AAACAACCAAAATTTTCTTATGA	94
79	20418	29331	3535	687444		Intron 3			T/A	T=58 A=42	GCAGAGTGCC\TTGGCTTGGCTGGGC	95
80	20524	29437	3641	687550		Intron 3			T/G	T=76 G=24	GCATGGCGGCTGACTTCCAAAAAGGG	96
81	20579	29492	3696	687605		Intron 3			G/A	G=50 A=50	CGCTTATTATGACTTCTGCTTGCAT	97
82	20618	29531	3735	687644		Intron 3			C/T	C=70 T=30	AAGCCAGTCA\CGTGGCTAAGTCTAG	98
89	21822	30735	4939	688848	413	Exon 4	130	S to S	T/C	T=60 C=40	GCTCAGACAG\CGGCCCCCACCACCAG	99
90	22104	31017	5221	689130		Exon 4 3' UTR			C/G	C=60 G=40	GGCGTCACAA\CAACCTGGTCAACAGG	100
91	22930	31843	6047	689956		Exon 4 3' UTR				insertion	CTCCCCCACC\AGGCTGGGAGCTCTG	101
93	23062	32206	6410	690319					T/C	T=68 C=32	GCAAAAAAGATATGGGGCAGCCTG	102
94	23293	32236	6440	690349					A/G	A=98 G=2	AACAGCCTCT\ACTGGAAACAACCCA	103
95	23323	31975	6179	690088					A/G	A=96 G=4	AAAGTTCCCT\ACTTCTCTGTGACTTC	104

FIGURE 11

FIGURE 14 A

# IL1A SNP Construct Genotypes

Constructs/SNP#	1	2	3	4	5	6	9	10	11	12	13	14	15	16	
pGL-AL4G	C	C	T	G	T	C	G	C	C	C	C	C	T	G	(SEQ ID NO: 105)
pGL-A1T		C	T	G	T	C	G	C	C	C	C	C	T	G	(SEQ ID NO: 106)
pGL-A2T	C		T	G	T	C	G	C	C	C	C	C	T	G	(SEQ ID NO: 107)
pGL-A3C	C	C		G	T	C	G	C	C	C	C	C	T	G	(SEQ ID NO: 108)
pGL-A4T	C	C	T		T	C	G	C	C	C	C	C	T	G	(SEQ ID NO: 109)
pGL-A5C	C	C	T	G		C	G	C	C	C	C	C	T	G	(SEQ ID NO: 110)
pGL-A6T	C	C	T	G	T		G	C	C	C	C	C	T	G	(SEQ ID NO: 111)
pGL3-IL1AL3X							G	C	C	C	C	C	T	G	(SEQ ID NO: 112)
pGL-A9A								C	C	C	C	C	T	G	(SEQ ID NO: 113)
pGL-A10T							G		C	C	C	C	T	G	(SEQ ID NO: 114)
pGL-A11T							G	C		C	C	C	T	G	(SEQ ID NO: 115)
pGL-A12T							G	C	C		C	C	T	G	(SEQ ID NO: 116)
pGL-A13T							G	C	C	C		C	T	G	(SEQ ID NO: 117)
pGL3-IL1AL3SX															(SEQ ID NO: 118)
pGL-A14T													T	G	(SEQ ID NO: 119)
pGL-A15A												C		G	(SEQ ID NO: 120)
pGL-A16A												C	T		(SEQ ID NO: 121)

FIGURE 15 A

# IL1B SNP Construct Genotypes

Constructs/SNP#	1	2	3	4	5	6	7	8	9	10	14	15	17	
pGL3-IL1BS	T	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:122)	
pGL-B1C	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:123)	
pGL3-IL1BS3KM	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:124)	
pGL-B2C	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:125)	
pGL-B3A	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:126)	
pGL-B4T	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:127)	
pGL-B5G	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:128)	
pGL-B6C	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:129)	
pGL-B7G	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:130)	
pGL-B8A	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:131)	
pGL-B9A	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:132)	
pGL-B10C	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:133)	
pGL-B14T	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:134)	
pGL-B15C	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:135)	
pGL3-IL1BL3KM	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:136)	
pGL-B17T	C	T	G	C	A	T	A	G	G	G	C	T	(SEQ ID NO:137)	

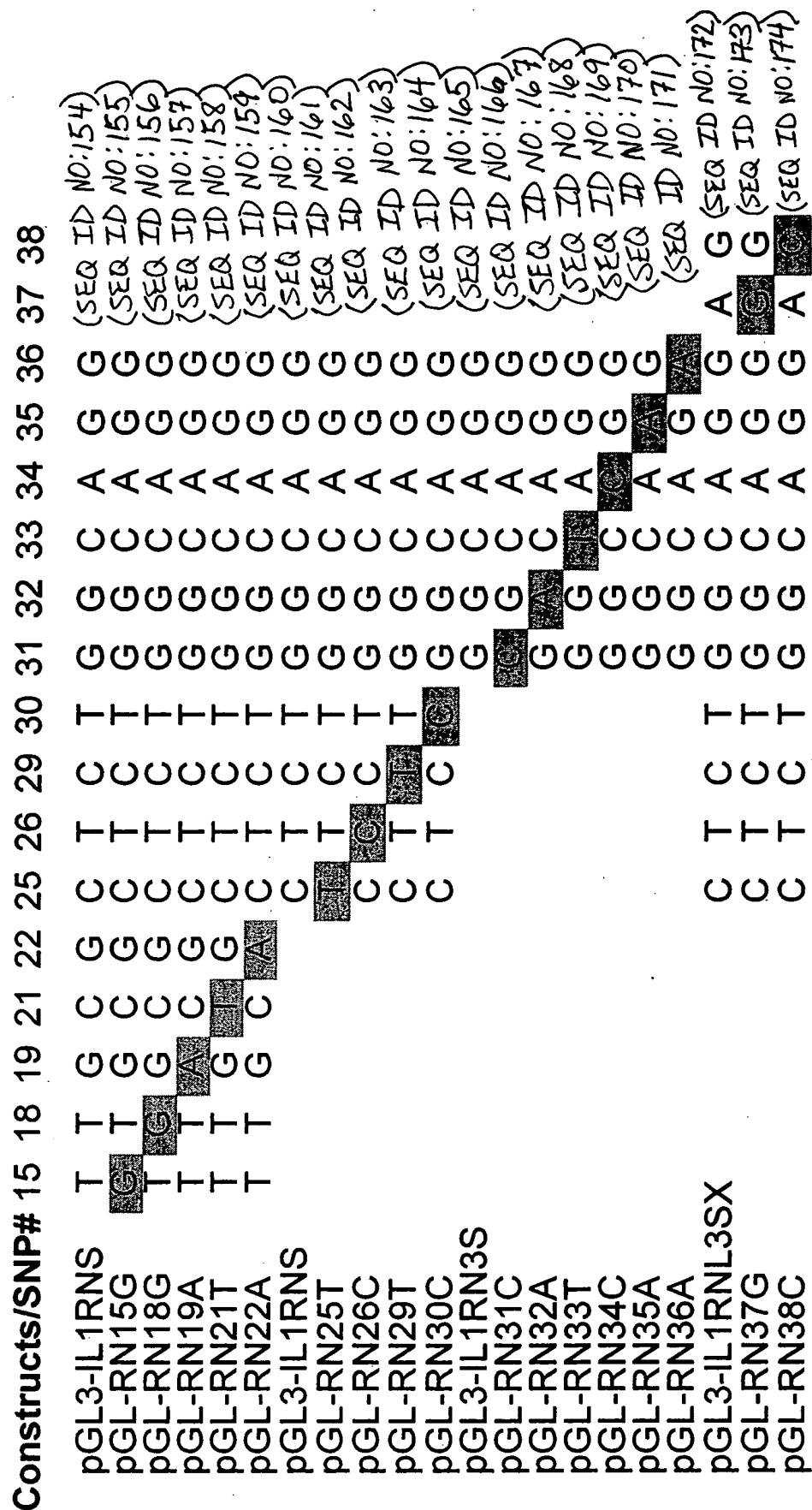
FIGURE 15 C

18 1B Promoter SNP Constructs (Allele 2 at 14 and 15)																		
Constructs	SNP #	1	2	3	4	5	6	7	8	9	10	14	15	17				
pGL-BB.2		T	T	G	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:138)			
pGL-B1C.2		C	T	G	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:139)			
pGL-BBK.2			T	G	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:140)			
pGL-B2C.2			C	G	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:141)			
pGL-B3A.2			T	A	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:142)			
pGL-B4T.2			T	G	T	A	T	A	G	G	G	T	T	C	(SEQ ID NO:143)			
pGL-B5G.2			T	G	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:144)			
pGL-B6C.2			T	G	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:145)			
pGL-B7G.2			T	G	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:146)			
pGL-B8A.2			T	G	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:147)			
pGL-B9A.2			T	G	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:148)			
pGL-B10C.2			T	G	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:149)			
pGL-B14T.2			T	G	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:150)			
pGL-B15C.2			T	G	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:151)			
pGL-BLK.2			T	G	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:152)			
pGL-B17T.2			T	G	C	A	T	A	G	G	G	T	T	C	(SEQ ID NO:153)			



FIGURE 16 A

# IL1RN SNP Construct Genotypes



Gene: <i>IL1A</i> ( <i>IL1F1</i> )			Orientation: Reversed	
Position	Exon	Exon boundaries	Type	
065938-067002	IL1A-7	<u>GAGATGCTGAGATA-ACATTAATTACCTTG</u>	CE3 + 3'	(SEQ ID NO:175)
069496-069620	IL1A-6	<u>TGAAATTGACATGG-CCAGTGCTGCTGAAG</u>	CE2	(SEQ ID NO:176)
071005-071175	IL1A-5	<u>AAATCATCAAGCCTA-ATCTGGATGAAGCAG</u>	PS + CE1	(SEQ ID NO:177)
073111-073333	IL1A-4	<u>AAATCCTTCTATCAT-ATGACTCAGAGGAAG</u>	PS	(SEQ ID NO:178)
074223-074271	IL1A-3	<u>TGAAATGAAGAAGA-CTGTCTCTGAATCAG</u>	PS	(SEQ ID NO:179)
075233-075287	IL1A-2	<u>AAGTCAAGATGGCCA-GAAGAAGCTGTTACAG</u>	5' + PS	(SEQ ID NO:180)
075952-076002	IL1A-1	<u>AAGTGCCAGCCAGA-TTTGAGTCAGCAAAG</u>	5'	(SEQ ID NO:181)
Coding Interleukin-1α				
cDNA sequence NM_000575, genomic sequence X03833.				
<i>IL1A</i> -1: $\emptyset$ <i>IL1A</i> -2: makypdmfed lkncys <sup>2</sup> (SEQ ID NO:182) <i>IL1A</i> -3: e <sup>3</sup> needsssid hlsing <sup>3</sup> (SEQ ID NO:183) <i>IL1A</i> -4: ksfyhvsygp lhegcmqsv slsissetskt skltfkesmv vvatngkvk krrlsisqsi tdddleaian dsee <sup>1</sup> (SEQ ID NO:184) <i>IL1A</i> -5: iikprsapfs flsnvkynfm riikkyefiln dalngsilra ndqyltaaal hnldeav <sup>1</sup> (SEQ ID NO:185) <i>IL1A</i> -6: kfdmgaykss kddakitvil risktqlvyt agdedqpvl k <sup>3</sup> (SEQ ID NO:186) <i>IL1A</i> -7: empeipkttit gsetnlffw ethgtknyft svahpnlfia tkqdywvcla gpppsitdf qlenqa <sup>3</sup> (SEQ ID NO:187)				

FIGURE 18 A

Gene: <i>IL1B</i> ( <i>IL1F2</i> )		Orientation: Reversed	
Position	Exon	Exon boundaries	Type
121295-122108	<i>IL1B-7</i>	<u>ACTGTAGATCCCAAA-TAAACTTCACTGAAG</u>	CE3 + 3'
122827-122957	<i>IL1B-6</i>	<u>TGGTGTCTCCATGT-ACTCTACAGCTGGAG</u>	CE2
124196-124360	<i>IL1B-5</i>	<u>AACTATCTTCTTCG-ATATGGAGCAACAAG</u>	PS + CE1
124908-125109	<i>IL1B-4</i>	<u>TGCTCCTTCCAGGAC-TCATCTTTGAAGAAG</u>	PS
127099-127150	<i>IL1B-3</i>	<u>TGGCAATGAGGATGA-CCTAAACAGATGAAG</u>	PS
127715-127777	<i>IL1B-2</i>	<u>GTGTCTGGAAGCAGC-GATGGCTTATTACAG</u>	5' + PS
128240-128311	<i>IL1B-1</i>	<u>ACCAACCTCTTCGAG-ATCTTCATTGCTCAA</u>	5'

Coding Interleukin-1β	
<i>IL1B</i> , from cDNA sequence M15330 and genomic sequence X04500.	
<i>IL1B</i> -1: ∅	
<i>IL1B</i> -2: maevpklae mmayy <sup>2</sup> (SEQ ID NO:195)	
<i>IL1B</i> -3: gnehdlffea dgpkqmk <sup>3</sup> (SEQ ID NO:196)	
<i>IL1B</i> -4: csfqdlclcp ldggqlris dhyskgfrq aasvvamdk lrkmlvpcp <sup>4</sup> tfqendlatf fpfifeee <sup>5</sup> (SEQ ID NO:197)	
<i>IL1B</i> -5: piffdtwdnq ayvhdapvrs lnctlrdsqg kslvmsgpye lkahlhggqd meqgv <sup>6</sup> (SEQ ID NO:198)	
<i>IL1B</i> -6: vfmsfvqge esndkipval alkeknlvys cvlkddkptl qle <sup>7</sup> (SEQ ID NO:199)	
<i>IL1B</i> -7: svdpknypkk kmekpfvfnk ieinnklefe saqfnwvys tsqaenmpvf lggtkgggdi	
tdftmqfvss * (SEQ ID NO:200)	

FIGURE 18 B

Gene: <i>IL1F7</i>		Orientation: Forward	
Position	Exon	Exon boundaries	Type
204598-204721	IL1F7-b1/c1	CTTCATTCATTTC-AGTCTGCTTAGAAG	5+PS?
205420-205482	IL1F7-b2/c2	ACCCGGCTGAAGCC-ATTTTGTTCACACAA	PS?
<206821-206887	IL1F7-a1	..ATGTCAGGCTGTGAT-AGAAGCGCTTAAGAG	PS?
208769-208888	IL1F7-a2/b3	GTCCAAAGGTGAAGA-ACTACATACGCCCAG	CE1
209275- 209417	IL1F7-a3/b4/c3	AGATCTTCTTTGTCAT-TCCCTTCAGCTGAAG	CE2
210204- 210529	IL1F7-a4/b5/c4	AAGGAGAACTGATG-AACCTGCTCACTAAA	CE3 + 3'
Coding			
Different cDNAs: IL-1F7a (AF201832), IL-1F7b (AF200496) and IL-1F7c (AF251120).			
IL1F7-b1/c1:	msfvngsgv kmgsedwekd epqcclcd	(SEQ ID NO: 207)	(SEQ ID NO: 201)
IL1F7-b2/c2:	pagspiepgp slptmfvht	(s/k): (SEQ ID NO: 208)	(SEQ ID NO: 202)
IL1F7-a1:	msgcdrrcte tkgknsfkkr lig	(SEQ ID NO: 209)	(SEQ ID NO: 203)
IL1F7-a2/b3:	pkvkninpkk fsihdqdhkv lvidsgnlia vpdknyirpe	(SEQ ID NO: 210)	(SEQ ID NO: 204)
IL1F7-a3/b4/c3:	iffalassls sasaekgspi llgvskgfvc lycdkdkgqs hlqlk	(SEQ ID NO: 211)	(SEQ ID NO: 205)
IL1F7-a4/b5/c4:	kekmlklaaq kesaripfif yraqvgswnm lesaahpgwf ictscncnep		(SEQ ID NO: 206)
	vgvtdkfenr khiefsfqpv ckaemsevsd *	(SEQ ID NO: 212)	

FIGURE 18 C

Gene: IL1F9			Orientation: Forward	
Position	Exon	Exon boundaries	Exon type	
269711-269760	IL1F9-1	GAGCCAGGATTCAGT-ACCCTTTCTTGCCAG	5'	(SEQ ID NO:213)
270302-270375	IL1F9-2	GTGCTGAGACAACCA-CCGTCATCAATCAA	5' + CS	(SEQ ID NO:214)
270903-271007	IL1F9-3	TGTGTAAACCTATTATTA-ACAGTGTGACCCAG	CE1	(SEQ ID NO:215)
271691-271830	IL1F9-4	TCACGTGTTGCTGTGTTA-ACATTGCAGCTAAAA	CE2	(SEQ ID NO:216)
276523-277335	IL1F9-5	GAGCAGAAGATCATG-CTAAAACTGATATAA	CE3 +3'	(SEQ ID NO:217)
Coding				
cDNA sequences AF200492 and AF206696.				
IL1F9-1: Ø				
IL1F9-2: mrgtpgdadg ggravyqgm <sup>1</sup> (SEQ ID NO:218)				
IL1F9-3: ckpitgtind lngqwtlqg qnlvavprsd svtpv <sup>1</sup> (SEQ ID NO:219)				
IL1F9-4: tvaviteckyp ealeqgrgdp iylgigmpem clycekvgeq ptlqlk <sup>1</sup> (SEQ ID NO:220)				
IL1F9-5: eqkmdlyqg pepvksflfy raktgtstl esvafpdwfi asskrdqpii ltsehgksyn tafelnind* (SEQ ID NO:221)				

Gene: IL1F6			Orientation: Forward	
Position	Exon	Exon boundaries	Exon type	
<297556-297565	IL1F6-1?	..ATGGAAAAG	5' + CS	(SEQ ID NO:222)
297658-297771	IL1F6-2	CATTGAAAATGACA-ACCGTATGCTCTCCAG	CE1	(SEQ ID NO:223)
298282-298421	IL1F6-3	TCACTATTGCCCTTAA-ACACTGCAGCTGAAG	CE2	(SEQ ID NO:224)
299516->299728	IL1F6-4	GAAAAGGATATAATG-ACTATGCTGTTTAA...	CE3...	(SEQ ID NO:225)
Coding				
cDNA sequences AF201831.				
IL1F6-1: mefa <sup>1</sup> (SEQ ID NO:226)				
IL1F6-2: lkidtpqqs lqdinhrvv lqdtliavp rkdrmspv <sup>1</sup> (SEQ ID NO:227)				
IL1F6-3: tiallscrhv etlekdrnp iylglinglnl clmcakvgdq ptlqlk <sup>1</sup> (SEQ ID NO:228)				
IL1F6-4: ekdmdlyng pepvksflfy hsqgrnstf esvafpgwfi avsseggcpl iltqelgkan ttdfgltmlf * (SEQ ID NO:229)				

FIGURE 18 D

Gene: <i>IL1F8</i>		Orientation: Reversed	
Position	Exon	Exon boundaries	Exon type
<313785-314471	IL1F8-b6	<u>G</u> TAGAAAGAGTGG- <u>T</u> AGTTTTCCTCATGT	CS + 3'
317797-317926	IL1F8-b5	<u>C</u> TTGAGGCTCCCAA- <u>G</u> GGGAATAGGAGTGG	CS
<319597-319809	IL1F8-a5	<u>G</u> AAAAAATATCATG- <u>G</u> ATTCTGTGGAATAA...	CE3...
320633-320772	IL1F8-a4/b4	<u>T</u> CACTCTTCATTAA- <u>A</u> CTTTCAGCTTAAG	CE2
322742-322849	IL1F8-a3/b3	<u>G</u> GGAGGCAGCACCCA- <u>G</u> CAGCATTAAAGCTG	CE1
323391-323460	IL1F8-a2/b2	<u>C</u> CTCCTCACCACCAT- <u>T</u> CATGAACCCACAAC	5' + CS
344518->344570	IL1F8-a1/b1	<u>G</u> ACACGGGTTCCTCC- <u>C</u> TTCACTTTTCCTAG...	5'
Coding			
Different cDNAs: IL-1F8a (AF201833), and IL-1F8b (AF200494).			
IL1F8-a1/b1:	∅		
IL1F8-a2/b2:	<u>m</u> npg <sup>r</sup> (SEQ ID NO:237)		
IL1F8-a3/b3:	<u>e</u> aapksyair <u>d</u> srqmvw <sup>is</sup> <u>g</u> nsiaapls <u>r</u> sikp <sup>r</sup> (SEQ ID NO:238)		
IL1F8-a4/b4:	<u>l</u> hliacrdt <u>e</u> fsdkekg <sup>nm</sup> <u>v</u> ylgikgkdl <u>c</u> lfcae <sup>iqgk</sup> <u>p</u> tlql <sup>r</sup> (SEQ ID NO:239)		
IL1F8-a5:	<u>e</u> knimdl <sup>ve</sup> <u>k</u> kaqkpl <sup>ff</sup> <u>h</u> nkegst <sup>svf</sup> <u>q</u> svsyggw <sup>fi</sup> <u>a</u> tsttsq <sup>gpi</sup> <u>f</u> ltker <sup>g</sup> itn		
	<u>n</u> tnfyldsve * (SEQ ID NO:240)		
IL1F8-b5:	<u>l</u> qgsqdn <sup>igk</sup> <u>d</u> tcwklv <sup>gih</sup> <u>t</u> cinldv <sup>res</sup> <u>c</u> fmgtldq <sup>wg</sup> <u>i</u> qvg <sup>r</sup> (SEQ ID NO:241)		
IL1F8-b6:	<u>r</u> kkwkss <sup>fqh</sup> <u>h</u> hirkk <sup>kd</sup> <u>s</u> smrtni <sup>gmp</sup> <u>g</u> rm* (SEQ ID NO:242)		

(SEQ ID NO:230)  
(SEQ ID NO:231)  
(SEQ ID NO:232)  
(SEQ ID NO:233)  
(SEQ ID NO:234)  
(SEQ ID NO:235)  
(SEQ ID NO:236)

FIGURE 18 E

Gene: <i>IL1F5</i>		Orientation: Forward	
<u>Position</u>	<u>Exon</u>	<u>Exon boundaries</u>	<u>Exon type</u>
<350401-350445	IL1F5-b1	..AAGGAAGGAGGGAGA-GAAGGAGTGAATAAG 2483 5'	
350810-350943	IL1F5-a1	CGCTGGGAATCCTGC-AAGAACATTCTGAG 2484 5' + SORF	
351114-351169	IL1F5-a2/b2	GGGAGTCTACACCT-GGCCTGTGCTTCG 2485 5' + CS	
352555-352640	IL1F5-a3/b3	AATGAAGGACTCGGC-GGAGGTCATTAAAG 2486 CE1	
353827-353954	IL1F5-a4/b4	GTGAAGAGATCAGCG-ACTCTAACACTAGAG 2487 CE2	
354156-356451	IL1F5-a5/b5	CCAGTGAACATCATG-AGAAAGAGAAACAAA 2488 CE3 + 3'	

Coding:

Different cDNAs: IL-1F5a (AF186094 and AJ242737) and IL-1F5b (AJ242738).

IL1F5-b1:  $\emptyset$   
 IL1F5-a1: magrkdrgkrkegkge\*~~249~~  
 IL1F5-a2/b2: mvlsgalcfr\*250  
 IL1F5-a3/b3: mkdsalkvly lhnqllagg lhagkvikg\*251  
 IL1F5-a4/b4: eeisvvpnrw ldaslsplvl gvqggsqclis cvvgqeptlt le\*252  
 IL1F5-a5/b5: pvnimelylg akeskstffy rrdmgltsstf esaaypgwfl ctvpeadqpv  
 rltqlpengg wnapitdfyf qqcd\*253

FIGURE 18 F

**Gene: *IL1F10*****Orientation: Forward**

<u>Position</u>	<u>Exon</u>	<u>Exon boundaries</u>	<u>Exon type</u>
364023-364475	<i>IL1F10</i> -a1	GGCAGTGGGACTGGG-GGCAAGATACTACAT	5' + CS (SEQ ID NO: 254)
366034-366119	<i>IL1F10</i> -a2	AATTAAATATGCAGA-ACAACTGCTGTGCAG	CE1 (SEQ ID NO: 255)
366244-366555	* <i>IL1F10</i> -b1	GCTGTGGCCTCTCCT-TCCCTACAGCTGGAG	5' + CS + CE2 (SEQ ID NO: 256)
366428-366555	* <i>IL1F10</i> -a3	AGAAGATCTGCATAC-TCCCTACAGCTGGAG	CE2 (SEQ ID NO: 257)
366857-367553	<i>IL1F10</i> -a4/b2	GATGTGAACATTGAG-TTATTGTAAACCTCT	CE3 + 3'N (SEQ ID NO: 258)

**Coding**Different cDNAs: *IL-1F10a* (AF334755) and *IL-1F10b* (AY026753).

*IL1F10*-a1: mcslpmaryy i<sup>2</sup> (SEQ ID NO: 259)  
*IL1F10*-a2: ikyadqkaly trdgqllvgd pvadnccae<sup>1</sup> (SEQ ID NO: 260)  
 \**IL1F10*-b1: msssfllpepl pakslqhgvplsl dssslsl lekicilpnrg  
 lartkvpifl giqggsrcla cveteeglql e<sup>3</sup> (SEQ ID NO: 261)  
 \**IL1F10*-a3: kictlpnrgl drtkvpiflg iqggsrclac veteeglql e<sup>3</sup> (SEQ ID NO: 262)  
*IL1F10*-a4/b2: dvnieelykg geeatrftff qsssgsafrl eaaawpgwfl cgpaepqqpv  
 qltkeseart kfyfeqsw\* (SEQ ID NO: 263)

**Gene: *IL1RN (IL1F3)*****Orientation: Forward**

<u>Position</u>	<u>Exon</u>	<u>Exon boundaries</u>	<u>Exon type</u>
409176-409311	<i>IL1RN</i> -b1/c1	GGGCAGCTCCACCCT-TCCCCATGGCTTTAG	5' + CS (SEQ ID NO: 264)
411350-411412	<i>IL1RN</i> -c2	CTGACTTGATGAAG-ATGCTGACTCAAAGG	CS (SEQ ID NO: 265)
418888-419017	* <i>IL1RN</i> -a1	GCTGCAGTCACAGAA-GATGCAAGCCTTCAG	5' + SS (SEQ ID NO: 266)
418966-419017	* <i>IL1RN</i> -b2/c3	AGACGATCTGCCGAC-GATGCAAGCCTTCAG	CS (SEQ ID NO: 267)
420853-420941	<i>IL1RN</i> -a2/b3/c4	AATCTGGGATGTAA-ATGTCAATTTAGAAG	CE1 (SEQ ID NO: 268)
422321-422433	<i>IL1RN</i> -a3/b4/c5	AAAAGATAGATGTGG-AGACTCCAGCTGGAG	CE2 (SEQ ID NO: 269)
423932-425290	<i>IL1RN</i> -a4/b5/c6	GCAGTTAACATCACT-AATCTTGAAATGCC	CE3 + 3' (SEQ ID NO: 270)

**Coding: Interleukin-1 receptor antagonist**Different cDNAs: *pro-sIL-1ra* (form a, X52015), *icIL-1ra* (form b, M55646) and *icIL-1raII* (form c, X84348).

*IL1RN*-b1/c1: mal(e/a)<sup>1</sup> (SEQ ID NO: 271)  
*IL1RN*-c2: dlyeeggggg gegednadsk e<sup>1</sup> (SEQ ID NO: 272)  
 \**IL1RN*-a1: meicrglrsh litlllflfh seticrggrks skmqaf<sup>2</sup> (SEQ ID NO: 273)  
 \**IL1RN*-b2/c3: ticrggrks skmqaf<sup>2</sup> (SEQ ID NO: 274)  
*IL1RN*-a2/b3/c4: iwdvnqktfy lrnnqlvagylqgpnvnlee<sup>1</sup> (SEQ ID NO: 275)  
*IL1RN*-a3/b4/c5: kidvvpieph alflgihgk mclscvksge trlql e<sup>3</sup> (SEQ ID NO: 276)  
*IL1RN*-a4/b5/c6: avnitdlsen rkqdkrfafi rdsqpttsf esaacpgwfl ctameadqpvs  
 sltnmpdegv mvtkfyfqed e\* (SEQ ID NO: 277)

**FIGURE 18 G**